

SEP 16 2003

TECH CENTER 1600/



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/840,243C

DATE: 09/12/2003

TIME: 14:21:12

Input Set : A:\510CON\_US\_Seq\_List.txt

Output Set: N:\CRF4\09122003\I840243C.raw

3 <110> APPLICANT: Masternak, Krzyztof  
4 Reith, Walter  
5 Mach, Bernard  
7 <120> TITLE OF INVENTION: NEW TRANSCRIPTION FACTOR OF MHC CLASS II GENES,  
8 SUBSTANCES CAPABLE OF INHIBITING THIS NEW  
9 TRANSCRIPTION FACTOR AND MEDICAL USES OF THESE SUBSTANCES  
11 <130> FILE REFERENCE: 23135-510 CON  
13 <140> CURRENT APPLICATION NUMBER: 09/840,243C  
14 <141> CURRENT FILING DATE: 2001-04-24  
16 <150> PRIOR APPLICATION NUMBER: EP 98120085.0  
17 <151> PRIOR FILING DATE: 1998-10-24  
19 <160> NUMBER OF SEQ ID NOS: 24  
21 <170> SOFTWARE: PatentIn Ver. 2.1  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 40  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Artificial Sequence  
28 <220> FEATURE:  
29 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
31 <400> SEQUENCE: 1  
32 ccgtacgcgt ctagaccatg gagcttaccg agcctgcaga 40  
35 <210> SEQ ID NO: 2  
36 <211> LENGTH: 31  
37 <212> TYPE: DNA  
38 <213> ORGANISM: Artificial Sequence  
40 <220> FEATURE:  
41 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
43 <400> SEQUENCE: 2  
44 ttcgaattct cgagtgtctg agtccccggc a 31  
47 <210> SEQ ID NO: 3  
48 <211> LENGTH: 37  
49 <212> TYPE: DNA  
50 <213> ORGANISM: Artificial Sequence  
52 <220> FEATURE:  
53 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
55 <400> SEQUENCE: 3  
56 ccgtacgcgt ctagaccatg gagcccactc aggttgc 37  
59 <210> SEQ ID NO: 4  
60 <211> LENGTH: 32  
61 <212> TYPE: DNA  
62 <213> ORGANISM: Artificial Sequence  
64 <220> FEATURE:  
65 <223> OTHER INFORMATION: Description of Artificial Sequence:primer

P.6

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67 <400> SEQUENCE: 4
68 ttcgaattct cgagtgcctg ggttcagca gg 32
71 <210> SEQ ID NO: 5
72 <211> LENGTH: 30
73 <212> TYPE: DNA
74 <213> ORGANISM: Artificial Sequence
76 <220> FEATURE:
77 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
79 <400> SEQUENCE: 5
80 ccagctctag actccaccac tctcaccaac 30
83 <210> SEQ ID NO: 6
84 <211> LENGTH: 30
85 <212> TYPE: DNA
86 <213> ORGANISM: Artificial Sequence
88 <220> FEATURE:
89 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
91 <400> SEQUENCE: 6
92 ccttcgaatt ctcgctcttt tgccaggatg 30
95 <210> SEQ ID NO: 7
96 <211> LENGTH: 30
97 <212> TYPE: DNA
98 <213> ORGANISM: Artificial Sequence
100 <220> FEATURE:
101 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
103 <400> SEQUENCE: 7
104 gggtctctag attggcagca ctggggatag 30
107 <210> SEQ ID NO: 8
108 <211> LENGTH: 30
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
115 <400> SEQUENCE: 8
116 gctacgaatt ccagcagaca cagccaaaac 30
119 <210> SEQ ID NO: 9
120 <211> LENGTH: 69
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial Sequence
124 <220> FEATURE:
125 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
127 <400> SEQUENCE: 9
128 ccgtacgcgt ctagaatgga ttacaaagac gatgacgata agatggagct taccagcct 60
130 gcagaagac 69
133 <210> SEQ ID NO: 10
134 <211> LENGTH: 1345
135 <212> TYPE: DNA
136 <213> ORGANISM: Homo sapiens
138 <220> FEATURE:
139 <221> NAME/KEY: CDS

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140 <222> LOCATION: (418)..(1200)
142 <400> SEQUENCE: 10
143 acgcagggaa ggaggcacac ccgggggtgg cgcagtgagg agggggcgcg acggccagga 60
145 ggctggtgga ggcacacca ggcaggagag ggggaagaac tctctccctt tctgaacccc 120
147 cttttccttg agagacgagt tgggggagtc ctccacgcat taccactcg ggccgcaaaa 180
149 actcccttct ttagccctct gcccccgccc ttgcttataa gcctttgaga ccgcagaagg 240
151 gaccttggtg tggaacggga cggccaagag gaagccagat cgctgagggt ccggtctcca 300
153 gtttgccctc tgctatatcc attggaagag aaaagtttgt gacttgggcc cccaagtttt 360
155 gagagaactg ggctttcggc gcgggggggac agaggaggct cgtgggggagc tttcccc 417
157 atg gag ctt acc cag cct gca gaa gac ctc atc cag acc cag cag acc 465
158 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
159 1 5 10 15
161 cct gcc tca gaa ctt ggg gac cct gaa gac ccc gga gag gag gct gca 513
162 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
163 20 25 30
165 gat ggc tca gac act gtg gtc ctc agt ctc ttt ccc tgc acc cct gag 561
166 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
167 35 40 45
169 cct gtg aat cct gaa ccg gat gcc agt gtt tcc tct cca cag gca ggc 609
170 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
171 50 55 60
173 agc tcc ctg aag cac tcc acc act ctc acc aac cgg cag cga ggg aac 657
174 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
175 65 70 75 80
177 gag gtg tca gct ctg ccg gcc acc cta gac tcc ctg tcc atc cac cag 705
178 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
179 85 90 95
181 ctc gca gca cag ggg gag ctg gac cag ctg aag gag cat ttg cgg aaa 753
182 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
183 100 105 110
185 ggt gac aac ctc gtc aac aag cca gac gag cgc ggc ttc acc ccc ctc 801
186 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
187 115 120 125
189 atc tgg gcc tcc gcc ttt gga gag att gag acc gtt cgc ttc ctg ctg 849
190 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
191 130 135 140
193 gag tgg ggt gcc gac ccc cac atc ctg gca aaa gag cga gag agc gcc 897
194 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
195 145 150 155 160
197 ctg tcg ctg gcc agc aca ggc ggc tac aca gac att gtg ggg ctg ctg 945
198 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
199 165 170 175
201 ctg gag cgt gac gtg gac atc aac atc tat gat tgg aat gga ggg acg 993
202 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
203 180 185 190
205 cca ctg ctg tac gct gtg cgc ggg aac cac gtg aaa tgc gtt gag gcc 1041
206 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
207 195 200 205
209 ttg ctg gcc cga ggc gct gac ctc acc acc gaa gcc gac tct ggc tac 1089

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```

210 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
211      210      215      220
213 acc ccg atg gac ctt gcc gtg gcc ctg gga tac cgg aaa gtg caa cag 1137
214 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
215 225      230      235      240
217 gtg atc gag aac cac atc ctc aag ctc ttc cag agc aac ctg gtg ccc 1185
218 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
219      245      250      255
221 gct gac cct gag tga aggccgcctg ccgggggactc agacactcag ggaacaaaat 1240
222 Ala Asp Pro Glu
223      260
225 ggtcagccag agctgggggaa acccagaact gacttcaaag gcagcttctg gacaggtggt 1300
227 gggaggggac ccttcccaag aggaaccaat aaaccttctg tgcag 1345
230 <210> SEQ ID NO: 11
231 <211> LENGTH: 260
232 <212> TYPE: PRT
233 <213> ORGANISM: Homo sapiens
235 <400> SEQUENCE: 11
236 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
237 1      5      10      15
239 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
240      20      25      30
242 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
243      35      40      45
245 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
246      50      55      60
248 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
249 65      70      75      80
251 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
252      85      90      95
254 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
255      100      105      110
257 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
258      115      120      125
260 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
261      130      135      140
263 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
264 145      150      155      160
266 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
267      165      170      175
269 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
270      180      185      190
272 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
273      195      200      205
275 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
276      210      215      220
278 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
279 225      230      235      240
281 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro

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```

282          245          250          255
284 Ala Asp Pro Glu
285          260
294 <210> SEQ ID NO: 12
295 <211> LENGTH: 260
296 <212> TYPE: PRT
297 <213> ORGANISM: Homo sapiens
299 <400> SEQUENCE: 12
300 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
301   1          5          10          15
303 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
304          20          25          30
306 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
307          35          40          45
309 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
310          50          55          60
312 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
313   65          70          75          80
315 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
316          85          90          95
318 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
319          100          105          110
321 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
322          115          120          125
324 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
325          130          135          140
327 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
328 145          150          155          160
330 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
331          165          170          175
333 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
334          180          185          190
336 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
337          195          200          205
339 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
340          210          215          220
342 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
343 225          230          235          240
345 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
346          245          250          255
348 Ala Asp Pro Glu
349          260
352 <210> SEQ ID NO: 13
353 <211> LENGTH: 269
354 <212> TYPE: PRT
355 <213> ORGANISM: Murinae gen. sp.
357 <400> SEQUENCE: 13
358 Met Glu Pro Thr Gln Val Ala Glu Asn Leu Val Pro Asn Gln Gln Pro
359   1          5          10          15

```

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; Xaa Pos. 31,148,159